

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/581,431
Source: IEUP
Date Processed by STIC: 7/17/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

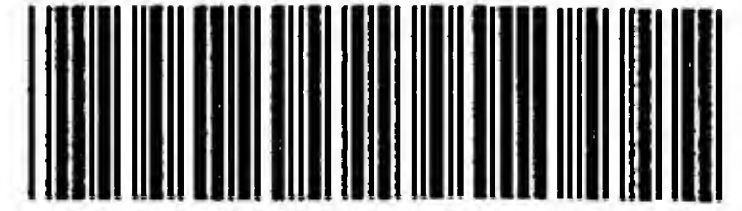
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Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/581,431

DATE: 07/17/2006

TIME: 11:00:20

Input Set : N:\RJAVED\10581431.txt

Output Set: N:\CRF4\07172006\J581431.raw

3 <110> APPLICANT: The Scripps Research Institute
 5 <120> TITLE OF INVENTION: INTEGRIN ALPHA.IIB.BETA.3 SPECIFIC ANTIBODIES AND PEPTIDES
 7 <130> FILE REFERENCE: TSRI1019.1PCT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/581,431
 C--> 9 <141> CURRENT FILING DATE: 2006-06-02
 9 <150> PRIOR APPLICATION NUMBER: US 60/526,859
 10 <151> PRIOR FILING DATE: 2003-12-03
 E--> 12 <160> NUMBER OF SEQ ID NOS: 24

ERRORED SEQUENCES

84 <210> SEQ ID NO: 9
 85 <211> LENGTH: 72
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 W--> 88 <220> FEATURE: n
 W--> 89 <221> NAME/KEY: a or g or c or t
 90 <222> LOCATION: 25,26,28,29,31,32,43,44,46,47,49,50
 91 <223> OTHER INFORMATION: encoded by randomized DNA sequence
 W--> 92 <400> SEQUENCE: 9
 W--> 93 gtgtattact gtgcgagagt ggggnknknk nnkcgtgccg acnnknknkn ktacgctatg 60
 E--> 95 gacgtctggg gc

97 <210> SEQ ID NO: 10
 98 <211> LENGTH: 21
 99 <212> TYPE: DNA
 100 <213> ORGANISM: Artificial Sequence

W--> 101 <220> FEATURE:
 W--> 101 <223> OTHER INFORMATION:
 W--> 101 <400> SEQUENCE: 10

E--> 102 agaagcgtag tccggaacgt c

104 <210> SEQ ID NO: 11
 105 <211> LENGTH: 57
 106 <212> TYPE: DNA
 107 <213> ORGANISM: Artificial Sequence

W--> 108 <220> FEATURE:
 W--> 108 <223> OTHER INFORMATION:
 W--> 108 <400> SEQUENCE: 11

E--> 109 gctgcccac cagccatggc cgaggtgcag ctgttgagg ctgggggagg cttggta 57

111 <210> SEQ ID NO: 12
 112 <211> LENGTH: 39
 113 <212> TYPE: DNA
 114 <213> ORGANISM: Artificial Sequence

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Input Set : N:\RJAVED\10581431.txt
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W--> 115 <220> FEATURE:
W--> 115 <223> OTHER INFORMATION:
W--> 115 <400> SEQUENCE: 12
E--> 116 cactctcgca cagtaataca cggccgtgtc ctcggtctc
118 <210> SEQ ID NO: 13
119 <211> LENGTH: 21
120 <212> TYPE: DNA
121 <213> ORGANISM: Artificial Sequence

W--> 122 <220> FEATURE:
W--> 122 <223> OTHER INFORMATION:
W--> 122 <400> SEQUENCE: 13

E--> 123 ggccatggct gggtgggcag c
125 <210> SEQ ID NO: 14
126 <211> LENGTH: 40
127 <212> TYPE: DNA
128 <213> ORGANISM: Artificial Sequence

W--> 129 <220> FEATURE:
W--> 129 <223> OTHER INFORMATION:
W--> 129 <400> SEQUENCE: 14

E--> 130 gaggaggag gaggaggaga gaagcgtagt ccggaacgtc
132 <210> SEQ ID NO: 15
133 <211> LENGTH: 24
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence

W--> 136 <220> FEATURE:
W--> 136 <223> OTHER INFORMATION:
W--> 136 <400> SEQUENCE: 15

E--> 137 aagacagcta tcgcgattgc agtg
139 <210> SEQ ID NO: 16
140 <211> LENGTH: 21
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence

W--> 143 <220> FEATURE:
W--> 143 <223> OTHER INFORMATION:
W--> 143 <400> SEQUENCE: 16

E--> 144 ggccatggct gggtgggcag c
146 <210> SEQ ID NO: 17
147 <211> LENGTH: 41
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence

W--> 150 <220> FEATURE:
W--> 150 <223> OTHER INFORMATION:
W--> 150 <400> SEQUENCE: 17

E--> 151 gaggaggagg aggaggaggc ggggcccagg cggccgagct c
153 <210> SEQ ID NO: 18
154 <211> LENGTH: 21
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence

W--> 157 <220> FEATURE:

See
error

39 explanation

on
pg 4.

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W--> 157 <223> OTHER INFORMATION:

W--> 157 <400> SEQUENCE: 18

E--> 158 ~~ggccatggtt-ggttgggcag c~~

266 <210> SEQ ID NO: 31

267 <211> LENGTH: 16

268 <212> TYPE: PRT

269 <213> ORGANISM: Artificial Sequence

W--> 270 <220> FEATURE:

W--> 270 <223> OTHER INFORMATION:

W--> 270 <400> SEQUENCE: 31

271 Val Gly Val Trp Cys Arg Ala Asp Lys Arg Cys Tyr Ala Met Asp

272 1 5 10 15

273 Val

E--> 278 41

see error explanation on page 4.

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see error explanation on pg. 4.

see error explanation
on page 1.

pls delete

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : N:\RJAVED\10581431.txt

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Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:1,2,4,5,6,7,8,10,11,12,13,14,15,16,17,18,20,21,23,24,25,26,27,28,29,30,31

VERIFICATION SUMMARY

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Input Set : N:\RJAVED\10581431.txt

Output Set: N:\CRF4\07172006\J581431.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:18 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
 ORGANISM:Artificial Sequence
 L:18 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
 ORGANISM:Artificial Sequence
 L:18 M:283 W: Missing Blank Line separator, <400> field identifier
 L:18 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:18
 L:26 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
 ORGANISM:Artificial Sequence
 L:26 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
 ORGANISM:Artificial Sequence
 L:26 M:283 W: Missing Blank Line separator, <400> field identifier
 L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:26
 L:34 M:283 W: Missing Blank Line separator, <220> field identifier
 L:34 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:38 M:283 W: Missing Blank Line separator, <400> field identifier
 L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
 L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
 ORGANISM:Artificial Sequence
 L:47 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
 ORGANISM:Artificial Sequence
 L:47 M:283 W: Missing Blank Line separator, <400> field identifier
 L:47 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:47
 L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
 ORGANISM:Artificial Sequence
 L:55 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
 ORGANISM:Artificial Sequence
 L:55 M:283 W: Missing Blank Line separator, <400> field identifier
 L:55 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:55
 L:63 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
 ORGANISM:Artificial Sequence
 L:63 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
 ORGANISM:Artificial Sequence
 L:63 M:283 W: Missing Blank Line separator, <400> field identifier
 L:63 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:63
 L:71 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
 ORGANISM:Artificial Sequence
 L:71 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
 ORGANISM:Artificial Sequence
 L:71 M:283 W: Missing Blank Line separator, <400> field identifier
 L:71 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:71
 L:79 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
 ORGANISM:Artificial Sequence
 L:79 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
 ORGANISM:Artificial Sequence
 L:79 M:283 W: Missing Blank Line separator, <400> field identifier
 L:79 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:79
 L:88 M:283 W: Missing Blank Line separator, <220> field identifier
 L:88 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:89 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
 L:92 M:283 W: Missing Blank Line separator, <400> field identifier
 L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0

L:95 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:72 SEQ:9
L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:101 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Artificial Sequence
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:101
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:10
L:108 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:108 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:108 M:283 W: Missing Blank Line separator, <400> field identifier

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L:108 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:108
 L:109 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:57 SEQ:11
 L:115 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
 ORGANISM:Artificial Sequence
 L:115 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
 ORGANISM:Artificial Sequence
 L:115 M:283 W: Missing Blank Line separator, <400> field identifier
 L:115 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:115
 L:116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:12
 L:122 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
 ORGANISM:Artificial Sequence
 L:122 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
 ORGANISM:Artificial Sequence
 L:122 M:283 W: Missing Blank Line separator, <400> field identifier
 L:122 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:122
 L:123 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:13
 L:129 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
 ORGANISM:Artificial Sequence
 L:129 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
 ORGANISM:Artificial Sequence
 L:129 M:283 W: Missing Blank Line separator, <400> field identifier
 L:129 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:129
 L:130 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:14
 L:130 M:252 E: No. of Seq. differs, <211> LENGTH:Input:40 Found:39 SEQ:14
 L:136 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
 ORGANISM:Artificial Sequence
 L:136 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
 ORGANISM:Artificial Sequence
 L:136 M:283 W: Missing Blank Line separator, <400> field identifier
 L:136 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:136
 L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:15
 L:143 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
 ORGANISM:Artificial Sequence
 L:143 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
 ORGANISM:Artificial Sequence
 L:143 M:283 W: Missing Blank Line separator, <400> field identifier
 L:143 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:143
 L:144 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:16
 L:150 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
 ORGANISM:Artificial Sequence
 L:150 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
 ORGANISM:Artificial Sequence
 L:150 M:283 W: Missing Blank Line separator, <400> field identifier
 L:150 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:150
 L:151 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:17
 L:157 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:18, <213>
 ORGANISM:Artificial Sequence
 L:157 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
 ORGANISM:Artificial Sequence
 L:157 M:283 W: Missing Blank Line separator, <400> field identifier
 L:157 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:157
 L:158 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:18
 L:164 M:283 W: Missing Blank Line separator, <400> field identifier

L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:172 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:172 M:283 W: Missing Blank Line separator, <400> field identifier
L:180 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:283 W: Missing Blank Line separator, <220> field identifier
L:188 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:192 M:283 W: Missing Blank Line separator, <400> field identifier
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:200 M:283 W: Missing Blank Line separator, <400> field identifier
L:208 M:283 W: Missing Blank Line separator, <400> field identifier

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L:216 M:283 W: Missing Blank Line separator, <400> field identifier
L:225 M:283 W: Missing Blank Line separator, <400> field identifier
L:234 M:283 W: Missing Blank Line separator, <400> field identifier
L:243 M:283 W: Missing Blank Line separator, <400> field identifier
L:252 M:283 W: Missing Blank Line separator, <400> field identifier
L:261 M:283 W: Missing Blank Line separator, <400> field identifier
L:270 M:283 W: Missing Blank Line separator, <400> field identifier
L:278 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:12 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (24) Counted (31)

